

SEQUENCE LISTING

<110> C. Frank Bennett
Kenneth W. Dobie

<120> ANTISENSE MODULATION OF MHC CLASS II TRANSACTIVATOR EXPRESSION

<130> RTS-0332

<160> 98

<210> 1

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 1

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<213> Artificial Sequence

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<223> Antisense Oligonucleotide

1005356, 10501

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<210> 3

<211> 6672

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (139)...(3531)

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gcatccttgg ggaagctgag ggcacgagga ggggctgccca gactccggga gctgctgcct 120

ggctgggatt cctacaca atg cgt tgc ctg gct cca cgc cct gct ggg tcc 171

Met Arg Cys Leu Ala Pro Arg Pro Ala Gly Ser

1

5

10

tac ctg tca gag ccc caa ggc agc tca cag tgt gcc acc atg gag ttg 219

Tyr Leu Ser Glu Pro Gln Gly Ser Ser Gln Cys Ala Thr Met Glu Leu

15

20

25

ggg ccc cta gaa ggt ggc tac ctg gag ctt ctt aac agc gat gct gac 267

Gly Pro Leu Glu Gly Gly Tyr Leu Glu Leu Leu Asn Ser Asp Ala Asp

30

35

40

ccc ctg tgc ctc tac cac ttc tat gac cag atg gac ctg gct gga gaa 315

Pro Leu Cys Leu Tyr His Phe Tyr Asp Gln Met Asp Leu Ala Gly Glu

45

50

55

gaa gag att gag ctc tac tca gaa ccc gac aca gac acc atc aac tgc 363

Glu Glu Ile Glu Leu Tyr Ser Glu Pro Asp Thr Asp Thr Ile Asn Cys

60

65

70

75

10006356 10501

gac cag ttc agc agg ctg ttg tgt gac atg gaa ggt gat gaa gag acc 411
 Asp Gln Phe Ser Arg Leu Leu Cys Asp Met Glu Gly Asp Glu Glu Thr
 80 85 90

agg gag gct tat gcc aat atc gcg gaa ctg gac cag tat gtc ttc cag 459
 Arg Glu Ala Tyr Ala Asn Ile Ala Glu Leu Asp Gln Tyr Val Phe Gln
 95 100 105

gac tcc cag ctg gag ggc ctg agc aag gac att ttc aag cac ata gga 507
 Asp Ser Gln Leu Glu Gly Leu Ser Lys Asp Ile Phe Lys His Ile Gly
 110 115 120

cca gat gaa gtg atc ggt gag agt atg gag atg cca gca gaa gtt ggg 555
 Pro Asp Glu Val Ile Gly Glu Ser Met Glu Met Pro Ala Glu Val Gly
 125 130 135

cag aaa agt cag aaa aga ccc ttc cca gag gag ctt ccg gca gac ctg 603
 Gln Lys Ser Gln Lys Arg Pro Phe Pro Glu Glu Leu Pro Ala Asp Leu
 140 145 150 155

aag cac tgg aag cca gct gag ccc ccc act gtg gtg act ggc agt ctc 651
 Lys His Trp Lys Pro Ala Glu Pro Pro Thr Val Val Thr Gly Ser Leu
 160 165 170

cta gtg gga cca gtg agc gac tgc tcc acc ctg ccc tgc ctg cca ctg 699
 Leu Val Gly Pro Val Ser Asp Cys Ser Thr Leu Pro Cys Leu Pro Leu
 175 180 185

cct gcg ctg ttc aac cag gag cca gcc tcc ggc cag atg cgc ctg gag 747
 Pro Ala Leu Phe Asn Gln Glu Pro Ala Ser Gly Gln Met Arg Leu Glu
 190 195 200

aaa acc gac cag att ccc atg cct ttc tcc agt tcc tcg ttg agc tgc 795
 Lys Thr Asp Gln Ile Pro Met Pro Phe Ser Ser Ser Ser Leu Ser Cys
 205 210 215

ctg aat ctc cct gag gga ccc atc cag ttt gtc ccc acc atc tcc act 843

411
 459
 507
 555
 603
 651
 699
 747
 795
 843

Leu Asn Leu Pro Glu Gly Pro Ile Gln Phe Val Pro Thr Ile Ser Thr
 220 225 230 235

ctg ccc cat ggg ctc tgg caa atc tct gag gct gga aca ggg gtc tcc 891
 Leu Pro His Gly Leu Trp Gln Ile Ser Glu Ala Gly Thr Gly Val Ser
 240 245 250

agt ata ttc atc tac cat ggt gag gtg ccc cag gcc agc caa gta ccc 939
 Ser Ile Phe Ile Tyr His Gly Glu Val Pro Gln Ala Ser Gln Val Pro
 255 260 265

cct ccc agt gga ttc act gtc cac ggc ctc cca aca tct cca gac cgg 987
 Pro Pro Ser Gly Phe Thr Val His Gly Leu Pro Thr Ser Pro Asp Arg
 270 275 280

cca ggc tcc acc agc ccc ttc gct cca tca gcc act gac ctg ccc agc 1035
 Pro Gly Ser Thr Ser Pro Phe Ala Pro Ser Ala Thr Asp Leu Pro Ser
 285 290 295

atg cct gaa cct gcc ctg acc tcc cga gca aac atg aca gag cac aag 1083
 Met Pro Glu Pro Ala Leu Thr Ser Arg Ala Asn Met Thr Glu His Lys
 300 305 310 315

acg tcc ccc acc caa tgc ccg gca gct gga gag gtc tcc aac aag ctt 1131
 Thr Ser Pro Thr Gln Cys Pro Ala Ala Gly Glu Val Ser Asn Lys Leu
 320 325 330

cca aaa tgg cct gag ccg gtg gag cag ttc tac cgc tca ctg cag gac 1179
 Pro Lys Trp Pro Glu Pro Val Glu Gln Phe Tyr Arg Ser Leu Gln Asp
 335 340 345

acg tat ggt gcc gag ccc gca ggc ccg gat ggc atc cta gtg gag gtg 1227
 Thr Tyr Gly Ala Glu Pro Ala Gly Pro Asp Gly Ile Leu Val Glu Val
 350 355 360

gat ctg gtg cag gcc agg ctg gag agg agc agc agc aag agc ctg gag 1275
 Asp Leu Val Gln Ala Arg Leu Glu Arg Ser Ser Ser Lys Ser Leu Glu

10006365 " 105004

365	370	375	
cgg gaa ctg gcc acc ccg gac tgg gca gaa cgg cag ctg gcc caa gga			1323
Arg Glu Leu Ala Thr Pro Asp Trp Ala Glu Arg Gln Leu Ala Gln Gly			
380	385	390	395
ggc ctg gct gag gtg ctg ttg gct gcc aag gag cac cgg cgg ccg cgt			1371
Gly Leu Ala Glu Val Leu Leu Ala Ala Lys Glu His Arg Arg Pro Arg			
400	405		410
gag aca cga gtg att gct gtg ctg ggc aaa gct ggt cag ggc aag agc			1419
Glu Thr Arg Val Ile Ala Val Leu Gly Lys Ala Gly Gln Gly Lys Ser			
415	420		425
tat tgg gct ggg gca gtg agc cgg gcc tgg gct tgt ggc cgg ctt ccc			1467
Tyr Trp Ala Gly Ala Val Ser Arg Ala Trp Ala Cys Gly Arg Leu Pro			
430	435		440
cag tac gac ttt gtc ttc tct gtc ccc tgc cat tgc ttg aac cgt ccg			1515
Gln Tyr Asp Phe Val Phe Ser Val Pro Cys His Cys Leu Asn Arg Pro			
445	450		455
ggg gat gcc tat ggc ctg cag gat ctg ctc ttc tcc ctg ggc cca cag			1563
Gly Asp Ala Tyr Gly Leu Gln Asp Leu Leu Phe Ser Leu Gly Pro Gln			
460	465	470	475
cca ctc gtg gcg gcc gat gag gtt ttc agc cac atc ttg aag aga cct			1611
Pro Leu Val Ala Ala Asp Glu Val Phe Ser His Ile Leu Lys Arg Pro			
480	485		490
gac cgc gtt ctg ctc atc cta gac gcc ttc gag gag ctg gaa gcg caa			1659
Asp Arg Val Leu Leu Ile Leu Asp Ala Phe Glu Glu Leu Glu Ala Gln			
495	500		505
gat ggc ttc ctg cac agc acg tgc gga ccg gca ccg gcg gag ccc tgc			1707
Asp Gly Phe Leu His Ser Thr Cys Gly Pro Ala Pro Ala Glu Pro Cys			
510	515		520

10005356-110501

tcc ctc cgg ggg ctg ctg gcc ggc ctt ttc cag aag aag ctg ctc cga 1755
 Ser Leu Arg Gly Leu Leu Ala Gly Leu Phe Gln Lys Lys Leu Leu Arg

525

530

535

ggt tgc acc ctc ctc ctc aca gcc cgg ccc cgg ggc cgc ctg gtc cag 1803
 Gly Cys Thr Leu Leu Leu Thr Ala Arg Pro Arg Gly Arg Leu Val Gln

540

545

550

555

agc ctg agc aag gcc gac gcc cta ttt gag ctg tcc ggc ttc tcc atg 1851
 Ser Leu Ser Lys Ala Asp Ala Leu Phe Glu Leu Ser Gly Phe Ser Met

560

565

570

gag cag gcc cag gca tac gtg atg cgc tac ttt gag agc tca ggg atg 1899
 Glu Gln Ala Gln Ala Tyr Val Met Arg Tyr Phe Glu Ser Ser Gly Met

575

580

585

aca gag cac caa gac aga gcc ctg acg ctc ctc cgg gac cgg cca ctt 1947
 Thr Glu His Gln Asp Arg Ala Leu Thr Leu Leu Arg Asp Arg Pro Leu

590

595

600

ctt ctc agt cac agc cac agc cct act ttg tgc cgg gca gtg tgc cag 1995
 Leu Leu Ser His Ser His Ser Pro Thr Leu Cys Arg Ala Val Cys Gln

605

610

615

ctc tca gag gcc ctg ctg gag ctt ggg gag gac gcc aag ctg ccc tcc 2043
 Leu Ser Glu Ala Leu Leu Glu Leu Gly Glu Asp Ala Lys Leu Pro Ser

620

625

630

635

acg ctc acg gga ctc tat gtc ggc ctg ctg ggc cgt gca gcc ctc gac 2091
 Thr Leu Thr Gly Leu Tyr Val Gly Leu Leu Gly Arg Ala Ala Leu Asp

640

645

650

agc ccc ccc ggg gcc ctg gca gag ctg gcc aag ctg gcc tgg gag ctg 2139
 Ser Pro Pro Gly Ala Leu Ala Glu Leu Ala Lys Leu Ala Trp Glu Leu

655

660

665

10006366 10006366

Cys Ala His Glu Ala Glu Glu Ala Gly Ile Trp Gln His Val Val Gln
 815 820 825

gag ctc ccc ggc cgc ctc tct ttt ctg ggc acc cgc ctc acg cct cct 2667
 Glu Leu Pro Gly Arg Leu Ser Phe Leu Gly Thr Arg Leu Thr Pro Pro
 830 835 840

gat gca cat gta ctg ggc aag gcc ttg gag gcg gcg ggc caa gac ttc 2715
 Asp Ala His Val Leu Gly Lys Ala Leu Glu Ala Ala Gly Gln Asp Phe
 845 850 855

tcc ctg gac ctc cgc agc act ggc att tgc ccc tct gga ttg ggg agc 2763
 Ser Leu Asp Leu Arg Ser Thr Gly Ile Cys Pro Ser Gly Leu Gly Ser
 860 865 870 875

ctc gtg gga ctc agc tgt gtc acc cgt ttc agg gct gcc ttg agc gac 2811
 Leu Val Gly Leu Ser Cys Val Thr Arg Phe Arg Ala Ala Leu Ser Asp
 880 885 890

acg gtg gcg ctg tgg gag tcc ctg cgg cag cat ggg gag acc aag cta 2859
 Thr Val Ala Leu Trp Glu Ser Leu Arg Gln His Gly Glu Thr Lys Leu
 895 900 905

ctt cag gca gca gag gag aag ttc acc atc gag cct ttc aaa gcc aag 2907
 Leu Gln Ala Ala Glu Glu Lys Phe Thr Ile Glu Pro Phe Lys Ala Lys
 910 915 920

tcc ctg aag gat gtg gaa gac ctg gga aag ctt gtg cag act cag agg 2955
 Ser Leu Lys Asp Val Glu Asp Leu Gly Lys Leu Val Gln Thr Gln Arg
 925 930 935

acg aga agt tcc tcg gaa gac aca gct ggg gag ctc cct gct gtt cgg 3003
 Thr Arg Ser Ser Ser Glu Asp Thr Ala Gly Glu Leu Pro Ala Val Arg
 940 945 950 955

gac cta aag aaa ctg gag ttt gcg ctg ggc cct gtc tca ggc ccc cag 3051
 Asp Leu Lys Lys Leu Glu Phe Ala Leu Gly Pro Val Ser Gly Pro Gln

10005356 110501
 10005356 110501

[illegible]

gtc cag gaa cac ctg caa caa cag gat tca cgg atc agc ctg aga tga 3531
 Val Gln Glu His Leu Gln Gln Gln Asp Ser Arg Ile Ser Leu Arg

1120

1125

1130

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10005355 11501

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 gagaatgaaa gggcccagag aggggtggtga cctctgcctg aagtcacaca gtgagtcgag 6471
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 caattctcat ttgtcacaca ctttggttat tagagatcaa ccccttcgct cctgtgtctt 6591
 gcaatggcag ccttggcaaa cgctaaatga aaatcgtgac aacacttggt ttatgaagca 6651
 tttactttgt gttcaccttg t 6672

<210> 4

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 4

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23

<210> 5

19

[illegible]

<210> 8

<211> 20

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> PCR Primer

<400> 8

gaagatggtg atgggatttc

20

<210> 9

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Probe

<400> 9

caagcttccc gttctcagcc

20

<210> 10

<211> 409

<212> DNA

<213> Homo sapiens

<220>

<400> 10

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60

gaa tac cac tgc act ctg ctc cat gag cct gat agt gag gct ctg gcc 379
Glu Tyr His Cys Thr Leu Leu His Glu Pro Asp Ser Glu Ala Leu Ala

[illegible]

40

45

50

agg aag atc tct ttg acc cta cta gag aaa gga gac ctg gat ttg gcc 427
 Arg Lys Ile Ser Leu Thr Leu Leu Glu Lys Gly Asp Leu Asp Leu Ala
 55 60 65 70

ctc ctg ggg tgg gcc cgg agt ggg ctg cag ccc cca gca gcc gag agg 475
 Leu Leu Gly Trp Ala Arg Ser Gly Leu Gln Pro Pro Ala Ala Glu Arg
 75 80 85

ggc ccc ggc cac agt gac cat ggt g 500
 Gly Pro Gly His Ser Asp His Gly
 90

<210> 12

<211> 429

<212> DNA

<213> Homo sapiens

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<221> promoter

<222> (1)...(354)

<400> 12

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 actcaggact tgcagatcac ttgccaagt ggctccctag ctcttggtc ctggcccggg 120
 gcctgggact ctcccgaag tggggctggc cactgtgagg aaccgactgg aggcagggac 180
 ctcttgatg cccaggcag ttgggatgcc acttctgata aagcacgtgg tggccacagt 240
 aggtgcttgg ttgctccaca gcctggccc agctcagcgc tgcagaaaga aagtgaagg 300
 gaaaaaagac tgcggggagg cggggaggta ggatgaccag cggacgagct gccacagact 360
 tgccgcggcc ccagagctgg cgggaggag aggccaccag cagcgcgcgc gggagcccgg 420
 ggaacagcg 429

10005365 "1050"

<210> 13

<211> 198

<212> DNA

<213> Homo sapiens

<220>

<221> promoter

<222> (1)...(134)

<400> 13

cccgggcgcc cgcctcagt ttcccatct ataaagtgga gatgataata gcattcagag	60
tactgatct aagggtcag ggacaccatt cagtgtgtaagc ccctgcaaga	120
ggaagctggt tctgactcag ccttgaggct ggcgtctgag gcaaccacaa gccaacgtg	180
catggtggaa agatgact	198

<210> 14

<211> 515

<212> DNA

<213> Homo sapiens

<220>

<221> exon:exon junction

<222> (66)...(67)

<400> 14

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gactcaggca gctcacagtg tgccaccatg gagttggggc ccctagaagg tggctacctg	120
gagcttctta acagcgatgc tgacccctg tgctcttacc acttctatga ccagatggac	180
ctggctggag aagaagagat tgagctctac tcagaacctg acacagacac catcaactgc	240
gaccagttca gcaggctgtt gtgtgacatg gaaggtgatg aagagaccag ggaggcttat	300
gccaatatcg cggaactgga ccagtatgtc ttccaggact ccagctgga gggcctgagc	360
aaggacattt tcatagagca cataggacca gatgaagtga tcggtgagag tatggagatg	420
ccagcagaag ttgggcagaa aagtcagaaa agacccttcc cagaggagct tccggcagac	480
ctgaagcact ggaagccagc tgagcccca ctgtg	515

tca gaa ccc gac aca gac acc atc aac tgc gac cag ttc agc agg ctg 358
Ser Glu Pro Asp Thr Asp Thr Ile Asn Cys Asp Gln Phe Ser Arg Leu

[illegible]

	70	75	80	
ttg tgt gac atg gaa ggt gat gaa gag acc agg gag gct tat gcc aat				406
Leu Cys Asp Met Glu Gly Asp Glu Glu Thr Arg Glu Ala Tyr Ala Asn				
	85	90	95	
atc gcg gaa ctg gac cag tat gtc ttc cag gac tcc cag ctg gag ggc				454
Ile Ala Glu Leu Asp Gln Tyr Val Phe Gln Asp Ser Gln Leu Glu Gly				
	100	105	110	
ctg agc aag gac att ttc ata gag cac ata gga cca gat gaa gtg atc				502
Leu Ser Lys Asp Ile Phe Ile Glu His Ile Gly Pro Asp Glu Val Ile				
	115	120	125	
ggt gag agt atg gag atg cca gca gaa gtt ggg cag aaa agt cag aaa				550
Gly Glu Ser Met Glu Met Pro Ala Glu Val Gly Gln Lys Ser Gln Lys				
	130	135	140	145
aga ccc ttc cca gag gag ctt ccg gca gac ctg aag cac tgg aag cca				598
Arg Pro Phe Pro Glu Glu Leu Pro Ala Asp Leu Lys His Trp Lys Pro				
	150	155	160	
gtg cct ttc tcc agt tcc tcg ttg agc tgc ctg aat ctc cct gag gga				646
Val Pro Phe Ser Ser Ser Ser Leu Ser Cys Leu Asn Leu Pro Glu Gly				
	165	170	175	
ccc atc cag ttt gtc ccc acc atc tcc act ctg ccc cat ggg ctc tgg				694
Pro Ile Gln Phe Val Pro Thr Ile Ser Thr Leu Pro His Gly Leu Trp				
	180	185	190	
caa atc tct gag gct gga aca ggg gtc tcc agt ata ttc atc tac cat				742
Gln Ile Ser Glu Ala Gly Thr Gly Val Ser Ser Ile Phe Ile Tyr His				
	195	200	205	
ggt gag gtg ccc cag gcc agc caa gta ccc cct ccc agt gga ttc act				790
Gly Glu Val Pro Gln Ala Ser Gln Val Pro Pro Pro Ser Gly Phe Thr				
	210	215	220	225

1006366 110501

gtc cac ggc ctc cca aca tct cca gac cgg cca ggc tcc acc agc ccc	838
Val His Gly Leu Pro Thr Ser Pro Asp Arg Pro Gly Ser Thr Ser Pro	
230 235 240	
ttc gct cca tca gcc act gac ctg ccc agc atg cct gaa cct gcc ctg	886
Phe Ala Pro Ser Ala Thr Asp Leu Pro Ser Met Pro Glu Pro Ala Leu	
245 250 255	
acc tcc cga gca aac atg aca gag cac aag acg tcc ccc acc caa tgc	934
Thr Ser Arg Ala Asn Met Thr Glu His Lys Thr Ser Pro Thr Gln Cys	
260 265 270	
ccg gca gct gga gag gtc tcc aac aag ctt cca aaa tgg cct gag ccg	982
Pro Ala Ala Gly Glu Val Ser Asn Lys Leu Pro Lys Trp Pro Glu Pro	
275 280 285	
gtg gag cag ttc tac cgc tca ctg cag gac acg tat ggt gcc gag ccc	1030
Val Glu Gln Phe Tyr Arg Ser Leu Gln Asp Thr Tyr Gly Ala Glu Pro	
290 295 300 305	
gca ggc ccg gat ggc atc cta gtg gag gtg gat ctg gtg cag gcc agg	1078
Ala Gly Pro Asp Gly Ile Leu Val Glu Val Asp Leu Val Gln Ala Arg	
310 315 320	
ctg gag agg agc agc agc aag agc ctg gag cgg gaa ctg gcc acc ccg	1126
Leu Glu Arg Ser Ser Ser Lys Ser Leu Glu Arg Glu Leu Ala Thr Pro	
325 330 335	
gac tgg gca gaa cgg cag ctg gcc caa gga ggc ctg gct gag gtg ctg	1174
Asp Trp Ala Glu Arg Gln Leu Ala Gln Gly Gly Leu Ala Glu Val Leu	
340 345 350	
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Leu Ala Ala Lys Glu His Arg Arg Pro Arg Glu Thr Arg Val Ile Ala	
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[illegible]

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Ala Leu Thr Leu Leu Arg Asp Arg Pro Leu Leu Leu Ser His Ser His
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agc cct act ttg tgc cgg gca gtg tgc cag ctc tca gag gcc ctg ctg 1846
Ser Pro Thr Leu Cys Arg Ala Val Cys Gln Leu Ser Glu Ala Leu Leu
565 570 575

gag ctt ggg gag gac gcc aag ctg ccc tcc acg ctc acg gga ctc tat 1894
Glu Leu Gly Glu Asp Ala Lys Leu Pro Ser Thr Leu Thr Gly Leu Tyr
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gtc ggc ctg ctg ggc cgt gca gcc ctc gac agc ccc ccc ggg gcc ctg 1942
Val Gly Leu Leu Gly Arg Ala Ala Leu Asp Ser Pro Pro Gly Ala Leu
595 600 605

gca gag ctg gcc aag ctg gcc tgg gag ctg ggc cgc aga cat caa agt 1990
Ala Glu Leu Ala Lys Leu Ala Trp Glu Leu Gly Arg Arg His Gln Ser
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acc cta cag gag gac cag ttc cca tcc gca gac gtg agg acc tgg gcg 2038
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1000333 110501

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880

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[illegible]

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Pro Phe Ala Pro Ser Ala Thr Asp Leu Pro Ser Met Pro Glu Pro Ala			
290	295	300	
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Leu Thr Ser Arg Ala Asn Met Thr Glu His Lys Thr Ser Pro Thr Gln			
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Cys Pro Ala Ala Gly Glu Val Ser Asn Lys Leu Pro Lys Trp Pro Gly			
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T0006366-110501

This image shows a vertical strip of a document page. On the left side, there is a dark, textured binding edge, likely from a book or a folder. The right side of the strip shows a white page area, which appears to be blank or has very faint, illegible text. The overall image is oriented vertically.

This image shows a vertical strip of a document page. On the left side, there is a dark, textured binding edge, likely from a book or a folder. The right side of the strip shows a white page area, which appears to be blank or has very faint, illegible text. The overall image is oriented vertically.

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This image shows a vertical strip of a document page. On the left side, there is a dark, textured binding edge, likely from a book or folder. The right side of the strip shows a white page area, which appears to be blank or has very faint, illegible text. The overall image is oriented vertically.



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RTS-0332 PATENT

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